

Amendments to the Drawings:

The attached 12 sheets of drawings include changes to Figs. 2, 6A-7:

Replacement Sheets 2/19-3/19 (Fig. 2), replace originally submitted sheets 2/19-3/19 (Fig. 2).

Replacement Sheets 7/19-13/19 (Figs 6A-6D), replace originally submitted sheets 7/19-13/19 (Figs. 6A-6D).

Replacement Sheets 14/19-16/19 (Fig. 7), replace originally submitted sheets 14/19-16/19 (Fig. 7).

The Amendments to the Drawings are made to incorporate the sequence identifier numbers. Applicant has submitted a “Marked-up” version of original sheets 2/19-3/19 and 7/19-16/19.

Attachment: 24 sheets of drawings, i.e., 12 “Replacement” and 12 “Marked-Up” sheets of drawings.

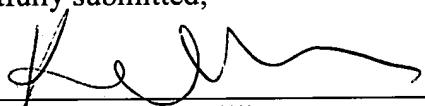
REMARKS

Applicants submit that the substitute specification and replacement drawings are filed simply to incorporate the sequence identifier numbers. No new matter is added.

Applicant submits that all claims are allowable as written and respectfully request early favorable action by the Examiner. If the Examiner believes that a telephone conversation with Applicant's attorney/agent would expedite prosecution of this application, the Examiner is cordially invited to call the undersigned attorney/agent of record.

Respectfully submitted,

Date: 3-30-2005


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2/19

FIGURE 2

Score = 553 bits (1425), Expect = e-156
 Identities = 327/700 (46%), Positives = 406/700 (57%), Gaps = 152/700 (21%)

Query: 1 **Sbjct:**

Beta-strand region	50	MSSRRWFHPTISGIEAEKLLQEQQFDGSFLARLSSSNPGAPTLSVRRGNEVTHIKIQNNG
Hydrogen bonded turn	48	M+SRRWFHP I+G+EAE LL +G DGSFLAR S SNPQ FTL SVRR VTHIKIQN G
Beta-strand region	41	MTSRRWFHPNITGVEAENLLLTRGVGDGSFLARPSKSNPQDFTLSVRRNGAVTHIKIQNNTG
Hydrogen bonded turn	38	*****
Beta-strand region	28	*****
Hydrogen bonded turn	26	**
Helical region	13	*****
Beta-strand region	7	*
SH2 1.	6	*****
Hydrogen bonded turn	5	**
PTPN11	1	*****

Query: 61 **Sbjct:**

Hydrogen bonded turn	61	DFFDLVGGEKPATLPELVQYYMEN-GELKEKNQAIELKQLICAEPPTTERWPHGNLSGK
Helical region	61	D++DLYGGEKPATL ELVQYYME+ G+LKEKNQ IELK PL CA+PT+ERWFHG+LSGK
Beta-strand region	83	DYYDLYGGEKPATLAELVQYYMEHHGQLKEKNQDVIELKYPLN CADPTSERWFHGHLSGK
Hydrogen bonded turn	74	*
Beta-strand region	70	*****
Hydrogen bonded turn	66	**
Beta-strand region	63	***
SH2 1.	61	*****
PTPN11	61	*****
Hydrogen bonded turn	85	**
Helical region	119	**
Beta-strand region	113	*
SH2 2.	112	*****
Hydrogen bonded turn	111	**
Hydrogen bonded turn	108	**
Beta-strand region	100	**
Beta-strand region	95	*
Beta-strand region	89	*

Query: 120 **Sbjct:**

Beta-strand region	120	EAEKLILERGKNGSPLVRESQS KPGDFVL SVRTDD-----KVTHVMIRWQDKKYD
Hydrogen bonded turn	120	EAEKL E+GK+GSFLVRESQS PGDFVL SVRT D KVTHVMIR Q+ KYD
Beta-strand region	121	EAEKL LLETEKGKHGSPLVRESQS HPGDFVL SVRT GESNDGSKVTHVMIR CQELKYD
Hydrogen bonded turn	147	*****
Beta-strand region	144	**
Hydrogen bonded turn	134	*****
Beta-strand region	132	**
Hydrogen bonded turn	129	*
Helical region	121	*****
SH2 2.	121	*****
PTPN11	121	*****
Beta-strand region	178	***
Hydrogen bonded turn	176	**
Beta-strand region	166	*****

Query: 170 **Sbjct:**

Helical region	170	VGGGESFGTLSELI DHYKRNP MVETCGTVVHLRQPFNATRITAAGINARVEQLVKGGFWE
Beta-strand region	181	VGGGE F +L++L++HYK+NPMVET GTV+ L+Q P N TRI A A +E V+
Beta-strand region	223	181 VGGGERFDSDLTDLV EHYKKKNPMVETL GTVLQLKQPLN TTRINA---AEIESRVR-----231
Beta-strand region	221	*
Beta-strand region	214	**
Beta-strand region	209	*
Hydrogen bonded turn	205	**
Beta-strand region	203	*
Helical region	190	*****
Beta-strand region	187	*
PTPN11	181	*****
SH2 2.	181	*****
Helical region	226	*****

Query: 230 **Sbjct:**

Helical region	230	EFESLQQDSRDTFSRNEG YKQENRLKNRYRNILPYDHTRVKLLDVEHSVAGAEYIN ANYI
Helical region	232	L + + T +G+ +E + LY ---ELS KLAETTD KVQGFWE EPETL QQEQCKLLYSRK E-----267
Helical region	256	232 -----
Helical region	256	*****
PTPN11	247	*****
Helical region	232	232 ++++++*****
Helical region	232	***

Query: 290 **Sbjct:**

290 RLPTDGDLYNMSSSES LNNSVPSCPACTAAQTQRNCNSNCQLQNKT CVCQCAVKSAILPYS	349
Q Q N + + N	ILP+

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3/19

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Sbjct:          268 -----GQRQENKKNRYKN-----ILPPD 286
Hydrogen bonded turn      280           ** 
PROTEIN-TYROSINE PHOSPHATASE. 276           *****   *****
Helical region      271           ***** 
PTPN11          268           ++++++*****+   +****+
Helical region      268           ** 
Hydrogen bonded turn      286           * 

Query:          350 NCATCSRKSDSLHKRSESSASSPSSGSGPGSSGTGVSSVNGPGTPTNLTSGTAG 409
                 +       D           P P +
Sbjct:          287 HTRVLHDGD-----PNEPV----- 302
Beta-strand region 289 *** 
Hydrogen bonded turn      287 ** 
PTPN11          287 ++++++*****+           +*****+
PROTEIN-TYROSINE PHOSPHATASE. 287 ***** 
Query:          410 CLVGLLKRHSNDSSGAVSISMAERERE-REREMPKTYIATQGCLLTQQVNTVDFWMW 468
                 D A + I M E E +   + K+YIATQGCL   NTV DFW MV+
Sbjct:          303 -----DYINA-NIIMPEFETKCNNSPKKSYIATQGCL-----NTVNDPWRMVF 346
Beta-strand region 304   *** 
PTPN11          303 ++++++*****+*****+*****+*****+*****+*****+
PROTEIN-TYROSINE PHOSPHATASE. 303 +*****+*****+*****+*****+*****+*****+*****+
Hydrogen bonded turn      335           *   ** 
Beta-strand region      327           *** 
Helical region      338           ***** 

Query:          469 QENTRIVMTTKEYERGKEKCARWPDEGRSEQFGHARIQCVSENSTSODYTLREFLVWR 528
                 QEN+RVIMTTKE ERKG KC +YWPDE   ++G R++ V E++ DYTLLRE +S
Sbjct:          347 QENSRVIVMTTKEVERGSKCVCVKYWPDEYALKEYGVMVRVNKESAADHTYTLRELKLSKV 406
Hydrogen bonded turn      406           * 
Beta-strand region      396           ***** 
Beta-strand region      383           ***** 
Hydrogen bonded turn      381           ** 
Beta-strand region      377           *** 
Hydrogen bonded turn      374           ** 
Beta-strand region      364           ** 
Hydrogen bonded turn      362           ** 
Beta-strand region      360           ** 
Beta-strand region      352           *** 
Hydrogen bonded turn      349           * 
Helical region      347 ** 
PTPN11          347 +*****+*****+*****+*****+*****+*****+*****+*****+*****+
PROTEIN-TYROSINE PHOSPHATASE. 347 ***** 
Query:          529 DQ--PARRIFHYHFQVWPDPDHGPADPGCVLNFLQDVNTRQSHLAQAGEKPGPICVHCSAG 586
                 Q   R ++ YHF WPDHGVP+DG VL+PL++V+ +Q   + AG   P+ VHCSAG
Sbjct:          407 GQQGNTERTVWQYHFRTWPDHGVPSPDPGGVLDFLEEVHHHQESIMDAG---PVVHCSAG 462
Beta-strand region 408   ***** 
Hydrogen bonded turn      407 * 
PTPN11          407 +*****+*****+*****+*****+*****+*****+*****+*****+*****+
PROTEIN-TYROSINE PHOSPHATASE. 407 +*****+*****+*****+*****+*****+*****+*****+*****+*****+
Hydrogen bonded turn      450           ** 
Helical region      432           ***** 
active          459           * 
Beta-strand region      455           *** 

Query:          587 IGRTGTFIVIDMILDQIVRNGLDTEIDIQRTIQMVRQRSGLQVTEAQYKFVYYAVQHYI 646
                 IGRTGTFIVID-+D I   G+D +ID+ +TIQMVRQRSG+VQTEAQY-F+Y AVQHYI
Sbjct:          463 IGRTGTFIVIDILIDIIREKGVDCCIDVPKTIQMVRQRSGMVQTEAQYRFIYMAVQHYI 522
Helical region      508           ***** 
Hydrogen bonded turn      502           ** 
Hydrogen bonded turn      499           ** 
Helical region      490           ***** 
Beta-strand region      487           ** 
Hydrogen bonded turn      484           ** 
Helical region      464           ***** 
PTPN11          463 +*****+*****+*****+*****+*****+*****+*****+*****+*****+
PROTEIN-TYROSINE PHOSPHATASE. 463 ***** 

Query:          647 QTLIARKRAEEQSLQVGREYTNIKYTGTIGIGNDSQRSPPLP 686
                 +TL R   E++S + G EYTNIKY+           +SPLPP
Sbjct:          523 ETLQRRIEEEQSKRKHGHEYTNIKYSLADQTSQDQSPPLP 562
Conflict        548           * 
phosphorylation 542           * 
Conflict        535           * 
Hydrogen bonded turn      524           * 
Helical region      523           * 
PTPN11          523 +*****+*****+*****+*****+*****+*****+*****+*****+

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7/19

FIGURE 6A

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 1

BLAST P sequence alignment

Score = 616 bits (1588), Expect = e-175
Identities = 306/517 (59%), Positives = 390/517 (75%), Gaps = 24/517 (4%)



Query: 453 QPGSRYASTNVLAAPVPPGTPRAVST-----EDITREPRITIQQKGPQGLGFNIVGGE 504
QP + S + P +P S + +ITREPR + + +G GLGFNIVGGE
Sbjct: 425 QPVNDHVSPPSFLGQTPASPARYSPVSKAVLGDDEITREPRKVVLHRGSTGLGFNIVGGE 484

(SEQ ID NO:281)

(SEQ ID NO:282)

Query: 505 DGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVLTHATHEAAQALKTSGGVVTLLAQ 564
DG+GI++SFILAGGPADL EL++GD+++SVN+V+L A+HE+AA ALK +G VT++AQ
Sbjct: 485 DGEGLFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAALKNAGQAVTIVAQ 544

Query: 565 YRPEEYNRFEARIQELKQQXXXXXXXXXXXX-XXQKRSLYVRALFDYDPNRDDGLPSRG 623
YRPEEY+RFEA+I +L++Q QKRSLYVRALFDYD +D GLPS+G
Sbjct: 545 YRPEEYSRFEAKIHDLRQMMNNSISSGSGSLRTSQKRSLYVRALFDYDKTKDGLPSQG 604

Query: 624 LPFKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDRSVKFQGH 683
L FK GDILHV NASDDEWWQAR+V D E +++G++PSKRR E+K RAR ++VKF
Sbjct: 605 LNFKFGDILHVINASDDEWWQARQVTPGESDEVGVIPSKRRVEKKERARLKTVKFN--- 661

Query: 684 AANNNLDKQSTLDRKKKNFTFSRKFPFMKSREDEKNDGSDQEPNGVVSSTSEIDIXXXX 743
+ DK + + K+K FSRKFPF K++D+ ++ SD + + V S+ S+ +
Sbjct: 662 --SKTRDKGQSFNDKRKKNLF SRKFPFYKNDQSEQETSDADQH-VTSNASDSE---- 712

Query: 744 XXXXXXXXXXXXVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYPDKGSCVPHTT 803
VLSYE V + +NYTRPVIILGP+KDRINDDLISE+PDKGSCVPHTT
Sbjct: 713 ---SSYRGQEEYVLSYEVPVNQQEVNYTRPVIILGPMKDRINDDLISEFPDKFGSCVPHTT 769

Query: 804 RPKREYEVGDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLGYTSVASVREVAEKGHCI 863
RPKR+YEVDGRDYHFV+SREQME+DIQ H FIEAGQYN++LYGTSV SVREVA KGKHC
Sbjct: 770 RPKRDYEVGDGRDYHFVTSREQMEKDIQEHKFIEAGQYNNHLYGTSVQSVREVAGKGKHC 829

Query: 864 LDVSGNAIKRLQVAQLYPVAVFIKPVSVDVMEMNRRMTEEQAKKTYERAIIKMEQEFGEY 923
LDVSGNAIKRLQ+AQLYP+++FIKPKS++++MEMN+R+TEEQA+KT+ERA+K+EQEF E+
Sbjct: 830 LDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNKLTEEQARKTFERAMKLEQEFTEH 889

Query: 924 FTGVVQGDTIEEYISKVSMIWSQSGPTIWPSKESL 960
FT +VQGDT+E+IY++VK + I QSG IWVP+KE L
Sbjct: 890 FTAIVQGDTLEDIYNQVKQIEEQSGSYIWVPAKEKL 926
Score = 206 bits (524), Expect = 2e-51
Identities = 119/227 (52%), Positives = 146/227 (63%), Gaps = 30/227 (13%)



Query: 24 LFNLD-----VNGDDS-WLYEDIQLERGNGLGFSIAGGTDNPHTGDTTSIYITKLIS 76
L N DS VNG D+ + YE+I LERGNGLGFSIAGGTDNPHTG D+SI+ITK+I+
Sbjct: 201 LVNTDSLETPTYVNNGTDADYEYEEITLERGNGLGFSIAGGTDNPHTGDDSSIFITKIIT 260

(SEQ ID NO:283)

(SEQ ID NO:284)

Query: 77 GGAAAADGRLXXXXXXXXXXXXXXXXXPHASAVIDALKKAGNVVKLHVKRXXXXXXXXX 136
GGAAA DGRL H+ AV+ALK+AG++V+L+VKR+
Sbjct: 261 GGAAAADGRLRVNDCILQVNEVDVRDVTHSKAVEALKEAGSIVRLYVKRRKPVE----- 315

Query: 137 XXXXXXXXXXXXKVIEIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRQAV 196

MARKED-UP VERSION

8/19

K++EI L+KG KGLGFSIAGG+GNQHIPGDN IYVTK+ +GG A
Sbjct: 316 -----KIMEIKLIKGPGLGFSIAGGVGNQHIPGDSIYVTKIIIEGAAHK 361

Query: 197 DGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIGK 243
DG+L IGDKL+AV + LE VTHE AV LK+ +D V L + K

Sbjct: 362 DGKLQIGDKLLAV---NNVCLEEVTHEEAVTALKNTSDFVYLVAK 404

Score = 88.2 bits (217), Expect = 7e-16

Identities = 68/234 (29%), Positives = 95/234 (40%), Gaps = 43/234 (18%)



Query: 40 DIQLERGNGLGFSIAGGTNDNPHIGTDTSIYITKLISGGAAAADGRXXXXXX 99
+I+L +G GLGFSIAGG N HI D SIY+TK+I GGAA DG+L

Sbjct: 319 EIKLIKGPGLGFSIAGGVGNQHIPGDSIYVTKIIIEGAAHKDGKLQIGDKLLAVNNVC 378

(SEQ ID NO:285)

(SEQ ID NO:286)

Query: 100 XXXXPHASAVDALKKAGNVVKLHVKRXXXXXXXXXXXXXKV----- 153
H AV ALK + V L V + V

Sbjct: 379 LEEVTHEEAVTALKNTSDFVYLVKAKPTSMYMNMDGYAPPDTINSSSQPVNDNHSPSSFLG 438

Query: 154 -----EIDLVGGKGLGFSIAGGIGNQHIPGDNGIYVT 186
++ L +G GLGF+I GG + GI+++

Sbjct: 439 QTPASPARYSPVSKAVLGDEITREPRKVVLHRGSTGLGFNIVCGEDGE-----GIFIS 492

Query: 187 KLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLI 240
+ GG A + G L GD++I+V + +L +HE A A LK+ VT++

Sbjct: 493 FILAGGPADLSGELRKGDRIISV---NSVDLRAASHEQAAAALKNAGQAVTIV 542

Score = 70.1 bits (170), Expect = 2e-10

Identities = 47/141 (33%), Positives = 69/141 (48%), Gaps = 12/141 (8%)



Query: 432 MPALPVESNQTNNRSQSPQRPGSRYASTNVLAAPPGTPRAVSTEDITREPRТИQK 491
+P LPV + T PQ P +T+ L TP V+ D E IT+++
Sbjct: 176 IPVLPVPAENTVILPTIPQANPPPV-LVNTDSLE-----TPTYVNGETADYEYEITLER 229

(SEQ ID NO:287)

(SEQ ID NO:288)

Query: 492 GPQGLGFNIVGGEDG-----QGIYVSFILAGGPADLGSELKRGDQLLSVNNVLTHATH 545
G GLGF+I GG D I+++ I+ GG A L+ D +L VN V++ TH
Sbjct: 230 GNSGLGFSIAGGTNDNPHIGDDSSIFITKIITGGAAAQDGRLRVNDCILQVNEVDVRDVTH 289

Query: 546 EEAAQALKTSGGVVTLLAQYR 566
+A +ALK +G +V L + R

Sbjct: 290 SKAVEALKEAGSIVRLYVKRR 310

Score = 67.4 bits (163), Expect = 1e-09

Identities = 39/81 (48%), Positives = 49/81 (60%), Gaps = 6/81 (7%)



Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVL 540
I + KGP+GLGF+I GG Q IYV+ I+ GG A +L+ GD+LL+VNNV L
Sbjct: 320 IKLIKGPGLGFSIAGGVGNQHIPGDSIYVTKIIIEGAAHKDGKLQIGDKLLAVNNVCL 379

(SEQ ID NO:289)

(SEQ ID NO:290)

Query: 541 THATHEEAQALKTSGGVTL 561
THEEA ALK + V L

Sbjct: 380 EEVTHEEAVTALKNTSDFVYL 400

MARKED-UP VERSION

9/19

FIGURE 6B

CLUSTAL W (1.82) sequence alignment

Drosophila Human	MTTRKKKRDGGSGGGFIKKVSSLFNLDSVNGDDSWLYEDIQLERGNGLGFSIAGGTDN MPVRKQD-----TQRALHLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ	47
Drosophila Human	PHIGTDTISIYTKLISGGAAAADGRSLINDIIVSVNDVSVVDPHASAVDALKAGNVK ALIDIQEYEVTLDDN--PKCID-RSKPSEPIQPVNTWEISSLPSSVTSETLPSSLSPS	120 104
Drosophila Human	LHVKRKRGTATTPAAGSAAGDARDSAASGPVIEIDLVKGKGKLGFSIAGGIGNQHIPGD VEKYRYQDEDTPPQEHIISP--QITNEVIGPELVHSEKN--LSEIENVHGFVSHSHIS-P	180 159
Drosophila Human	NGIYVTKLTDGGRAQVDGRSLIGDKLIAVRTNGSEKN--LENVTHELAVATLKSITDKV IKPTEAVLPSPPTVPVIPVLPVPAENTVILPTIPQANPPPVLVNTDSLETPTVNGTDAD	237 219
Drosophila Human	TLLIGKTQHLTTSA----GGGGGLLSSGQQQLSQSQSQLATSQSOSQVHQQQHATPMVNS YEYEEITLERGNGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAQDGRLRVNDCILQV	293 279
Drosophila Human	QSTGALNSMGQTVDSPSIPOAAAAAVAAAANASASAVIASNNTISNTTVTTVTATATAS NEVDVRDVTHSKAVEALKEAGSIVRLYVKRRKPVSEKIMEIK-LIKGPKGLGFSIAGGVG	353 338
Drosophila Human	NDSSKLPPSILGANSSISIANSNSNSNSNNINNINSINNNNSSSSSTTATVAAATPTAASA NQHIPGDNSIYVTKIIEGAAHKDGKLQIGDKLAVNNVCLEEEVTHEEAUTALKNTSDFV	413 398
Drosophila Human	AAAAASSPPANSFYNNASMPALPVESNQTNNRSQSPQPRQPGSRYASTNVLAAPVPGTPR YLKVAK-PTSMYMNDFGYAPPDITNSSQPVDNHVSPSS-FLGQTPASP---ARYSPVSKA	473 453
Drosophila Human	AVSTEDITREPRITIIQKGPGQGLGFNIVGGEDQGIYVFSFILAGGPADLGSELKRGDQLL VLGddeITREPRKVVLHRGSTGLGFNIVGGEDGEFIFISFILAGGPADLSGELRKGDRI	533 513
Drosophila Human	SVNNVNLTHATHEEEAAQALKTSGGVVTLAQYRPEEYNRFEARIQELKQQAALGAGGSGT SVNSVDLRAASHEQAAAALKNAGQAVTIVAQYRPEEYSRFEAKIHDLRQEMMNNSISSGS	593 573
Drosophila Human	-LLRTTQKRSLYVRALFDYDPNRDDGLPSRGLPFKHGDIHLHVTNASDDEWWQARRVLGDN GSLRTSQKRSLYVRALFDYDKTKDSGLPSQGLNFKFQDILHVINASDDEWWQARQVTPDG	652 633
Drosophila Human	EDEQIGIVPSKRRWERKMRARDRSVKFQGHAAANNNLDKQSTLDRKKNFTFSRKFPFMK ESDEVGVIPSKRRVEKKERARLKTVFN----SKTRDKGQSFNDKRKKNLFSRKFPFYK	712 688
Drosophila Human	SRDEKNEDGSQEPNGVSSSTSEIDINNNNNQSNEPQPSEENVLSYEAVQRSLISINYTRP NKDQSEQETSDADQH-VTSNASDSESSYRGQ-----EYVLSYEPVNQQEYVNYTRP	772 738
Drosophila Human	VIIGPLKDRINDDLISEYPDKFGSCVPHTTRPKREYEVGDRDYHFVSSREQMERDIQNH VIILGPMKDRINDDLISEFPDKFGSCVPHTTRPKRDYEVGDRDYHFVTSREQMEKDIQEH	832 798

MARKED-UP VERSION

10/19

MARKED-UP VERSION

11/19

FIGURE 6C

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 2

BLASTP sequence alignment

Score = 621 bits (1601), Expect = e-176
Identities = 318/524 (60%), Positives = 390/524 (73%), Gaps = 43/524 (8%)



MARKED-UP VERSION

12/19

Query: 142 XXXXXXXXXVIEIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRQVDGRLS 201
V+EI L KG KGLGFSIAGG+GNQHIPGDN IYVTK+ DGG AQ DGRL
Sbjct: 191 -----VVEIKLFKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGAAQKDGLRQ 240

Query: 202 IGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIG 242
+GD+L+ V + LE VTHE AVA LK+ ++ V L +G
Sbjct: 241 VGDRLLMV---NNYSLEEVTHEEAVAILKNTSEVVYLKVG 277
Score = 66.2 bits (160), Expect = 3e-09
Identities = 40/125 (32%), Positives = 64/125 (51%), Gaps = 11/125 (8%)

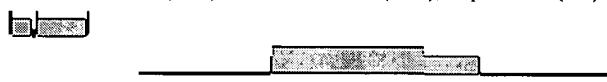


Query: 448 SPQPRQPQRSRYASTNVLAAPPGTPRAVSTEDITREPRTITIQKGPQGLGFNIVGGEDGQ 507
SP P +T+ L +P V+ +I E IT+++G GLGF+I GG D
Sbjct: 65 SPLKASPAPIIVNTDLDTIP----YVNGTEIEYEFEITLERGNNSGLGFSIAGGTNDNP 119

(SEQ ID NO:295)
(SEQ ID NO:296)

Query: 508 -----GIYVSFILAGGPADLGSELKRGDQLLSVNNVLTHATHEEEAQALKTSGGVVTL 561
GI+++ I+ GG A L+ D +L VN V+++ +H +A +ALK +G + L
Sbjct: 120 HIGDDPGIFITKIIIPGGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARL 179

Query: 562 LAQYR 566
+ R
Sbjct: 180 YVRRR 184
Score = 65.5 bits (158), Expect = 5e-09
Identities = 38/81 (46%), Positives = 47/81 (57%), Gaps = 6/81 (7%)



Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVL 540
I + KGP+GLGF+I GG Q IVV+ I+ GG A L+ GD+LL VNN +L
Sbjct: 194 IKLFKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGAAQKDGLRQVGDRLLMVNNYSL 253

(SEQ ID NO:297)
(SEQ ID NO:298)

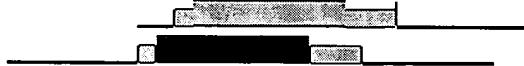
Query: 541 THATHEEEAQALKTSGGVVTL 561
THEEE LK + VV L
Sbjct: 254 EEVTHEEAVAILKNTSEVVYL 274
Score = 50.8 bits (120), Expect = 1e-04
Identities = 33/87 (37%), Positives = 48/87 (54%), Gaps = 10/87 (11%)



Query: 154 EIDLVKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRQVDGRLSIGDKLIAVRTNG 213
++ L KG GLGF+I GG + GI+V+ + GG A + G L GD+++V NG
Sbjct: 421 KVVLHKGSTGLGFNIVGGEDGE-----GIFVSFILAGGPADLSGELQRGDQILSV--NG 472

(SEQ ID NO:299)
(SEQ ID NO:300)

Query: 214 SEKNLENVTHELAVATLKSITDKVTLI 240
+ L +HE A A LK VT+I
Sbjct: 473 ID--LRGASHEQAAAALKGAGQTVTII 497
Score = 41.2 bits (95), Expect = 0.10
Identities = 24/81 (29%), Positives = 36/81 (43%), Gaps = 6/81 (7%)



Query: 41 IQLERGNNSGLGFSIAGGTDNPHIGTDTISIYITKLISGGAAAADGRLXXXXXXXXXXXX 100
+ L +G++GLGF+I GG D I+++ +++GG A G L
Sbjct: 422 VVLHKGSTGLGFNIVGGEDG-----EGIFVSFILAGGPADLSGELQRGDQILSVNGIDL 475

(SEQ ID NO:301)
(SEQ ID NO:302)

Query: 101 XXXPHASAVIDALKKAGNVVKL 121
H A ALK AG V +
Sbjct: 476 RGASHEQAAAALKGAGQTVTI 496

MARKED-UP VERSION
13/19

FIGURE 6D

CLUSTAL W (1.82) sequence alignment

Drosophila	-----MTTRKKKR DGG-----	11	(SEQ ID NO:261) (SEQ ID NO:303)
Human	MFFAC YCALRTNVKKYRYQDEDAPHDSL PRLTHEVRGPELVHVSEKNLSQIENVHGYVL	60	
Drosophila	-----GS GGGFIKKVSSLFNLDSVNG-DDSWLYEDIQLERGNGLGFSIAGGT DNP-----	62	
Human	QSHISPLKASPAPII VNTDLDTIPVNGTEIEYE FEEITLERGNGLGFSIAGGT DNP-----	120	
Drosophila	IGDTDSIYITKLISGGAAAADGR LSINDIIVSVNDVS VVDVPHAS AVDALKAGNVV KLH-----	122	
Human	IGDDPGIFITKIIPGGAAAEDGR LRVNDCIL RVNEVDVSEVSHSKA EALKEAGSIAR LY-----	180	
Drosophila	VKRKRG TATTPAAGSAAGDARD SAASGP KVI EIDL VKGK GLGFSIAGGIGNQH I PGDNG-----	182	
Human	VRRR RPILE T-----VVEIKL FKPGK GLGFSIAGGVGNQH I PGDNS-----	221	
Drosophila	IYVTKLTDGGRAQVDGR LSIGDKLIAVR NGSEKNLENVTHELA VATLKSITDKVTLIIG-----	242	
Human	IYVTKIIDGGAAQKDGR LQVGDR LLMVNN---YSLEEVTHEEAVAILKNTSEVVYLKVG-----	277	
Drosophila	KTQH LTT SASGGGGGLSSGQQQLSQSQLATSQS QSVHQQQHATPMVNSQSTGALNSM-----	302	
Human	NPTTI YM TD PYGP-----PDITHS-----YSPPMEN-----	303	
Drosophila	GQTVDSPS IPQAAA AVAAA N ASASVIA SNNT ISNTT VTV TATA S NDSSKL PPS-----	362	
Human	HLLSGNN-----GTLEYKTSL PPI S-----	323	
Drosophila	LGANSSISI SNSNSNSNSNNINNINSINNNN SSSSTTATVAA ATPTA ASAAAAAASSPP-----	422	
Human	PGRYSPIPK HMLV DDDYTRPPEPV STVN KLC DP-----ASPRH YSPV ECDKSF LL-----	375	
Drosophila	ANSFYNNA SMPALP VESN QTNNR SQSP QPRQ PGSR YASTNV LAAV PPGT PRAVSTE DITR-----	482	
Human	S-APYSHYHLGLLP-----DSEM TS HSQH STATRQP-----SMTL QRAV SLE-----G-----	417	
Drosophila	EPR TITI QKG P QGLGF NI VGG EGDQ GQI YV SF ILAGG PADLG SELK RDQ DQLL SVNN VN LTH-----	542	
Human	EPR KV VLHK G STGLGF NI VGG EGDGE G IFV SF ILAGG PADLG SELQ RDQ ILSV NGID LR-----	477	
Drosophila	ATHEEEA A QALK TSGG VVTLLA QYR PEE YNR FEAR I QELK QQA ALGAGG SGT-----LL RTT QKR-----	601	
Human	ASHEQ AAA ALK GAG QTVT II AQY QP EDY ARFEAKI HDL REQM MNH S MSSG SGSL RTN QKR-----	537	
Drosophila	SLY VR ALF DYDP NR DDGL PSL RGL PFKH GDIL HVTN AS DDEW QARR VLG DNE DEQ I GIV P-----	661	
Human	SLY VR AMF DYDK SKD GS GLP S QGL SF KY GDIL HV IN AS DDEW QARR VM LEGD SEEM GIV P-----	597	
Drosophila	SK RRWER KMR ARDRS VKF QGH AA ANN NL DK QST LDR KK NFT FSR KFP FM KS RDE KNE DG-----	721	
Human	SK RRVER KER AR LKTV KF NAK PG VID-----SK GS FND KR K S F IFS R KFP FY KN KE QSE QET-----	655	
Drosophila	SDQE P N G VVS STSE I DI NN VNN N QSN EP QP S EEN VLS YEA V QRL S IN YTRP VI ILG PLK D-----	781	
Human	SDPE-----RG QED LIL SYEP VTR QEI NYTRP VI ILG PMKD-----	691	
Drosophila	RIN DDL ISE YPD KFG SCV PHT TRPK REY EVD GRD YHF VSS RE QM ERDI QNHL FIE AGQ YN-----	841	
Human	RIN DDL ISE FPD KFG SCV PHT TRPK RDY EVD GRD YHF VIS RE QM EK D I QEH K FIE AGQ YN-----	751	
Drosophila	DNLY GT SVAS VREVA EKG KH CILD VSG NAI KRL QVA QL YPV AVF I KPK SV DS VME MN RRM-----	901	
Human	DNLY GT SVQ S VRF VA ERG KH CILD VSG NAI KRL QVA QL YPI AFI KPK RS L E SLM EMN KRL-----	811	
Drosophila	TEEQAKK TYERA IKM E QEF G EY FTG VVQ G D TIE E I YSK V KSM I WS QSG P T I W VPS KES L-----	960	
Human	TEEQAKK TYD RA I KLE QEF G EY FT A IV QGD TLE D I YN QCK L V I F E QSG P F I W P S K E K L-----	870	

MARKED-UP VERSION
14/19

FIGURE 7

Hu-Dlg1	--MPVRKQDTQRALHLLVEYRSKLSQTEDRQLRSSIERVINIFQNSNLFO-ALIDIQEYF	56
Hu-Dlg4	--MSQRPRAPRSALWLLAPPLLRWAPP-----LLTVLHSDFQ-ALLDILDYY	45
Hu-Dlg2	--MFFACCYCALRTNVKKYRYQDEDAPHDHS-----LPRLTHEVRGP-ELHVSEK-	47
Hu-Dlg3	MHKHQHCKCPCPECYEVTRALAALRRLEPPGYG-----DWQVPDPYGPGGNGASAGYGGYS	55
Dm-Dlg1	--MTTRKK-----KRDGG-----	111
Hu-Dlg5	--	
 Hu-Dlg1		
Hu-Dlg4	EVTLLDNPKCIDRSKPSEPIQPVNTWEISSLPSSVTSETLPSSLSPSVEKYRYQDEDTP	116
Hu-Dlg2	EASLSES-----	QKYRYQDEDTP 63
Hu-Dlg3	NLSQIEN-----	VHGIVLQSHISP 66
Dm-Dlg1	SQTLPSQAG-----	ATPTPRTKAKLIP 77
Hu-Dlg5	--	
 Hu-Dlg1		
Hu-Dlg4	PQEHIISPQITNEVIGPELVHVSEKNLSEIENVHGFVSHSHISPIKPTEAVLPSPPTVPI	176
Hu-Dlg2	PLEHSP-----	AHLPN-----
Hu-Dlg3	LK-----	68
Dm-Dlg1	TGRDVG-----	PVPLKPVPGK 93
Hu-Dlg5	--	
 Hu-Dlg1		
Hu-Dlg4	PVLPPAENTVILPTIPQANPPPVLVNTDSLETPI--TYVNGTDADYEYEEITLERGN	233
Hu-Dlg2	-----QANSPPPVIVNTDTLEAPGYELQVNTEGEMEYEEITLERGN	117
Hu-Dlg3	-----ASPAPIIVNTDTLDTIP---YVNGTEIEYEFEEITLERGN	107
Dm-Dlg1	-----STPKLNGSGPSWWPECTCTNRDWYEQVNNGSDGMFKYEEIVL	140
Hu-Dlg5	-----GSGGGFIKKVSSLNFNLD---SVNGDD-SWLYEDIQLERGN	49
	-----MRATHGSNSLPPSSARLGSSSN 21	
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 Hu-Dlg1		
Hu-Dlg4	LGFSIAGGTNDPHIGDDSSIFITKIITGGAAAQDGRLRVNDCLIQVNEVDVDRDTHSKAV	293
Hu-Dlg2	LGFSIAGGTNDPHIGDDPSIFITKIIPGGAAAQDGRLRVNDSLIFVNEVDVREVTHSAAV	177
Hu-Dlg3	LGFSIAGGTNDPHIGDDPGIFITKIIPGGAAAEDGRLRVNDCLIRVNEVDVSEVSHSKAV	167
Dm-Dlg1	LGFSIAGGTNDPHIGDDPGIFITKIIPGGAAAAMDGRLGVNDCVLVRNEVEVSEVVHSRAV	200
Hu-Dlg5	LGFSIAGGTNDPHIGDTTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAV	109
	LQFKAER-IKIPSTPRYPRSVVGSER--GSVSHSECSTPPQSPLNIDTLSSCSQSQTSA 78	
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 Hu-Dlg1		
Hu-Dlg4	EALKEAGSIVRLYVKRRK-----PVS-----EKIMEIKLIKGPKGFLGFSI	333
Hu-Dlg2	EALKEAGSIVRLYVMRRK-----PPA-----EKVMEIKLIKGPKGFLGFSI	217
Hu-Dlg3	EALKEAGSISARLYVRRRK-----PIL-----ETVVEIKLFKGPKGLGFSI	207
Dm-Dlg1	EALKEAGPVVRLVVRQQ-----PPP-----ETIMEVNLLKGPKGLGFSI	240
Hu-Dlg5	DALKKAGNVVKLVHKRKR-GTATTPAAGSAAGDARDSAASGPKVIEIDLVLVKGKGLGFSI	168
	TLPRIAVNPASLGERRKD-----PYV-----EEPRHVKVQKGSEPLGSI	119
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 Hu-Dlg1		
Hu-Dlg4	AGGVGNQHI PGDNSIYVTKIEGGAAHKDGKLQIGDKLLAVNN---VCLEEVTHEEAVT	389
Hu-Dlg2	AGGVGNQHI PGDNSIYVTKIEGGAAHKDGRLQIGDKILAVNS---VGLEDVMHEDA	273
Hu-Dlg3	AGGVGNQHI PGDNSIYVTKIIDGGAAQDGRLQVGDRLLMVNN---YSLEEVTHEEAVA	263
Dm-Dlg1	AGGIGNQHI PGDNSIYVTKIEGGAAQDGRLQIGDRLLAVNN---TNLQDVRHEEAVA	296
Hu-Dlg5	AGGIGNQHI PGDNGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKLNLENVTHELAVA	228
	VSGE-----KGGIYVSKVTVGSIAHQAG-LEYGDQLLEFNG---INLRSATEQQARL	167
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 Hu-Dlg1		
Hu-Dlg4	ALKNTSDFVYVLKVAKPSTSMMNDGYA-----	415
Hu-Dlg2	ALKNTYDVYVLKVAKPNSAYLSDSYA-----	299
Hu-Dlg3	ILKNTSEVYVLKVGNPTTIYMTDPYG-----	289
Dm-Dlg1	SLKNTSDMVYLKVAKPGSLHLNDMYA-----	322
Hu-Dlg5	TLKSITDKVTLIIGKTQHLLTSASGGGGGLSSGQQSQLATSQSOSQVHQHQHAT	288
	IIGQQCDTTILAQYNPHVHQLSSH-----	193
	: . . : :	
 Hu-Dlg1		
Hu-Dlg4	--	
Hu-Dlg2	--	
Hu-Dlg3	--	
Dm-Dlg1	--	
 Hu-Dlg1		
Hu-Dlg4	PMVNSQSTGALNSMGQTVVDSPSIPQAAAAVAAAANASASASVIASNNNTISNTT	348
Hu-Dlg2	TTVTA	
Hu-Dlg3		
Dm-Dlg1		

MARKED-UP VERSION

15/19

Hu-Dlg5

Hu-Dlg1	-----PP-----DITNSSSQPVDNHVS-----PSSFLG----- 438
Hu-Dlg4	-----PP-----DITTSYSQHLDNEIS-----HSSYLGTD-----YP 326
Hu-Dlg2	-----PP-----DITHSYSPPMENHLL-----SGNNGTLE-----YK 316
Hu-Dlg3	-----PP-----DYASTFTALADNHIS-----HNSSLGYLGAVESKVSY 356
Dm-Dlg1	TATASNDSSKLPPSLGANSSISISNSNSNSNNINNINSINNNNSSSSTTATVAAATP 408
Hu-Dlg5	-----RSSSHLDPAUTHSTLQ-----GSGTTTPEHPSVIDPLM 226
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Hu-Dlg1	--QTAPASPARSPVSKAVLGDDETR----- 462
Hu-Dlg4	TAMTPTSPRRYSPVAKDLLGEEDIPIR----- 352
Hu-Dlg2	TSLPPISPGRYSPIPKHMVLVDDDYTRPPEPVYSTVNKLCDKPASPRHSPVECDKSFLS 376
Hu-Dlg3	PAPPVPPTRYSPIPRMLAEDFTR----- 382
Dm-Dlg1	TAASAAAAASSPANSFYNNASAMPALPVESNQTNNRSQPQPRQPGSRYASTN----- 462
Hu-Dlg5	EQDEGPSTPPAKQSSSRAGDANKKT----- 252
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Hu-Dlg1	-----EPRKVVLHRGSTGLGFNIV 481
Hu-Dlg4	-----EPERRIVIHRGSTGLGFNIV 371
Hu-Dlg2	APYSHYHLGLLPDSEMTSHSQHSTATRQPSMTLQRAVSLEGEPRKVVLHKGSTGLGFNIV 436
Hu-Dlg3	-----EPRKIIILHKGSTGLGFNIV 401
Dm-Dlg1	-----VLAAVPPGTPRAVSTEDITREPRTITIQKGPGQLGFNIV 501
Hu-Dlg5	-----LEPRVVFIKKSQLLELGVHLC 272
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Hu-Dlg1	GGEDGEGERIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAAALKNAGQAVTI 541
Hu-Dlg4	GGEDGEGERIFISFILAGGPADLSGELRKGDQILSVNGVDLNRNASHEQAAIAALKNAGQVTI 431
Hu-Dlg2	GGEDGEGERIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQVTI 496
Hu-Dlg3	GGEDGEGERIFVSFILAGGPADLSGELRGRDRILSVDNGVNLNATHEQAAAALKRAGQSVTI 461
Dm-Dlg1	GGEDQQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTATHTHEEEAQALKTSGGVVTL 561
Hu-Dlg5	GG-NLHGVFVAEVEDDSPAKGPDGLVPGDLILEYGSLDVRNKTVVEEVYVEMLKPRDGVR 331
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Hu-Dlg1	VAQYRPEEYSRFEAKIHDLRQMMNISSSGSGSLRTSQKRSLYVRALFDYDKTKDSGLP 601
Hu-Dlg4	IAQYKPEEYSRFEAKIHDLRQLMNSSLGSGTASLRSNPKRGFYIRALFDYDKTKDCGFL 491
Hu-Dlg2	IAQYQPEDYARFEAKIHDLRQMMNHSMSGGSGSLRTNQKRSLYVRAMFDYDKSKDGLP 556
Hu-Dlg3	VAQYRPEEYSRFESKIHDLRQMMNMSGGSGSLRTSEKRSLYVRALFDYDRTRDSCP 521
Dm-Dlg1	LAQYRPEEYNRFEARIQELKQQAALGAGGSGT-LLRTTQKRSLYVRALFDYDPNRDDGLP 620
Hu-Dlg5	KVQYRPEEFTKAKG-----LPGDSFYIRALYDR-----LADV 363
. : * : * : : : .. * : * : : : * ; *** : : . * :	
Hu-Dlg1	SQGLNFKFGDILHVINASDD--EWWQARQVTPDGESDEVGVIPSKRVEREKKERARLKV 658
Hu-Dlg4	SOALSFRFGDVHLVIDASDE--EWWQARRVHSSETDDIGFIPSKRVEREWSRLKAK 548
Hu-Dlg2	SQGLSFKYGDILHVINASDD--EWWQARRVMLEGDSEEMGVIPSKRVEREKERARLKV 613
Hu-Dlg3	SQGLSFSYGDILHVINASDD--EWWQARLVTPHGESEQIYGIVPSKRVEREKERARLKV 578
Dm-Dlg1	SRGLPKHGDIHVNTNASDD--EWWQARRVLDNEDEQIYGIVPSKRWERKMRARDRSV 677
Hu-Dlg5	EQELSFKKDDILYVDDTLPQGTFGSWMAWQLDENAQKIQRGQIPSKYVMDQEFSRRLSMS 423
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Hu-Dlg1	KFNSKT----RDKGQSFDNDRKKNLFSRKFVFKYKNKDQSEQETSDADQH----- 703
Hu-Dlg4	DWG----- 551
Hu-Dlg2	KFNAKPGVI--DSKGSFDNDRKKSFIFSRKFVFKYKNKEQSEQE----- 654
Hu-Dlg3	KFHARTGMI--ESNRDFPGLSDDYY----- 601
Dm-Dlg1	KFQGHAAANNLKDQSTLDRKKNFTFSRKFPFMKSRDEKNEDGSDQEPMNGVVSSTSEID 737
Hu-Dlg5	EVKDDNSATKTLSSAARRSFFRKRKHKRSGSKDGKDLLALDAFS----- 468
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Hu-Dlg1	VTSNASDSESSYRGQEEYVLSYEPVNQQEVNYTRPVIILGPMKDRINDDLISEFPDKFGS 763
Hu-Dlg4	-----SSSGSQGREDSVLSYETVTQMEVHYARPIIILGPTKDRANDDLLSEFPDKFGS 604
Hu-Dlg2	-----TSDPERGQEDLILSYEPVTRQEINYTRPVIILGPMKDRINDDLISEFPDKFGS 707
Hu-Dlg3	-----GAKNLKGQEDAILSYEPVTRQEINYHYARPVIIILGPMKDRVNDDLISEFPDKFGS 654
Dm-Dlg1	INNVNNNQSNEPQPSSEENVLSYEAQRSLINYTRPVIILGPKLDRINDDLISEYFPDKFGS 797
Hu-Dlg5	-----SDSIPLFEDSVSLAYQRVQKVDCTALRPVLILGPLLDVVVKEMLVNEAPGKFCR 521
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Hu-Dlg1	CVPHTTRPKRDYEVGDRDYHFVTSREQMEKDIQEHKFIEAGQYNNHLYGTSVQSVREVAG 823
Hu-Dlg4	CVPHTTRPKREYEIDGRDYHFVSSREKMEKDIQAHKFIEAGQYNSHLYGTSVQSVREVAE 664
Hu-Dlg2	CVPHTTRPKRDYEVGDRDYHFVISREQMEKDIQEHKFIEAGQYNDLYGTSVQSVRFAE 767
Hu-Dlg3	CVPHTTRPDRDNEVGQDHYFVVSREQMEKDIQDNKFIEAGQFNDNLGTSIQSVRRAAE 714
Dm-Dlg1	CVPHTTRPKREYEVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDLYGTSVAVSVREVAE 857
Hu-Dlg5	CPLEVMK-----ASQQAIERGVKDCLFVDYKRRSGHFVDVVTVTASIXEITE 566
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MARKED-UP VERSION
16/19

Hu-Dlg1	KGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNK-----RLTEEQARKTFE 877
Hu-Dlg4	QGKHCLLDVSANAVRRLQAAHLHPIAIFIRPRSLENVLEINK-----RITEEQARKAFD 718
Hu-Dlg2	RGKHCLLDVSGNAIKRLQVAQLYPIAIFIKPKSLESLMMENK-----RLTEEQAKKTYD 821
Hu-Dlg3	RGKHCLLDVSGNAIKRLQQAQLYPIAIFIKPKSIEALMEMNR-----RQTYEQANKIYD 768
Dm-Dlg1	KGKHCLLDVSGNAIKRLQVAQLYPVAVFIKPKSVDVMEMNR-----RMTEEQAKKTYE 911
Hu-Dlg5	KNRHCLLDIAPHAIERLHHMHYPIVIFIHYKSAKHIKEQRDPYLRDKVTQRHSKEQFE 626
	: : * : * : : : * : : : * : : * . : * . : * . : * . : :
Hu-Dlg1	RAMKLEQEFTEHFTAIVQGDTLEDIYNQVKQIIIEQSGSYIWVPAKEKL 926
Hu-Dlg4	RATKLEQEFTECFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWVPARERL 767
Hu-Dlg2	RAIKLEQEFGHEYFTAIVQGDTLEDIYNQCKLVIEEQSDFIWIIPSKEKL 870
Hu-Dlg3	KAMKLEQEFGHEYFTAIVQGDSLEEYNIKIKQIIEDQSGHYIWVPSPEKL 817
Dm-Dlg1	RAIKMEQEFGHEYFTGVVQGDTIEBIYSKVSMIWSQSGPTIWVPSKESL 960
Hu-Dlg5	AAQKLEQEYSRYFTGVIQGGALSSICTQILAMVNQEQNKLWIPACPL- 674
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